OIPE

RAW SEQUENCE LISTING   DATE: 01/17/2002
PATENT APPLICATION: US/10/034,500   TIME: 16:04:12

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   3 <110> APPLICANT: JACOBS, Antonius A.C.
   4   VERMEIJ, Paul
   6 <120> TITLE OF INVENTION: LAWSONIA INTRACELLULARIS VACCINE
   8 <130> FILE REFERENCE: JACOBS ET AL.
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/034,500
  11 <141> CURRENT FILING DATE: 2001-12-20
  13 <150> PRIOR APPLICATION NUMBER: EP00204660.5
  14 <151> PRIOR FILING DATE: 2000-12-20
  16 <160> NUMBER OF SEQ ID NOS: 20
  18 <170> SOFTWARE: PatentIn Ver. 2.1
  20 <210> SEQ ID NO: 1
  21 <211> LENGTH: 656
  22 <212> TYPE: DNA
  23 <213> ORGANISM: Lawsonia intracellularis
  25 <220> FEATURE:
  26 <221> NAME/KEY: CDS
  27 <222> LOCATION: (1)..(654)
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  31 Ala Glu Val Thr Ala Ser Cys Thr Lys Arg Val Glu Ser Tyr Asn Tyr
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  34 ctt gtg gat tat tca ggc tct atg atg atg aaa cat gtt gct gtt aga   96
  35 Leu Val Asp Tyr Ser Gly Ser Met Met Met Lys His Val Ala Val Arg
  36   20   25   30
  38 gag cct aaa ata gaa tta gca aaa gaa gct ata tta aaa att aat gcg   144
  39 Glu Pro Lys Ile Glu Leu Ala Lys Glu Ala Ile Leu Lys Ile Asn Ala
  40   35   40   45
  42 gca atg cct aaa atg tca tat caa ggt gga tta tat act ttt gca cct   192
  43 Ala Met Pro Lys Met Ser Tyr Gln Gly Gly Leu Tyr Thr Phe Ala Pro
  44   50   55   60
  46 tat tct gta att att ccc caa ggt tct tgg aat tca tgt gtt gcc gaa   240
  47 Tyr Ser Val Ile Ile Pro Gln Gly Ser Trp Asn Ser Cys Val Ala Glu
  48 65   70   75   80
  50 tgt gcg gtt aat aca att aag tct gat tta gaa att ttt ggt cgt ctt   288
  51 Cys Ala Val Asn Thr Ile Lys Ser Asp Leu Glu Ile Phe Gly Arg Leu
  52   85   90   95
  54 act cct gtg gga gac ggc ata aaa atg cat gaa aca gtc att aat caa   336
  55 Thr Pro Val Gly Asp Gly Ile Lys Met His Glu Thr Val Ile Asn Gln
  56   100   105   110
  58 atg ccc cct cag gca gcc gtt att ctt ctc act gat ggt cat aat aat   384
  59 Met Pro Pro Gln Ala Ala Val Ile Leu Leu Thr Asp Gly His Asn Asn
  60   115   120   125
  62 tta ggg atg aat cct gtt gag gaa gta aaa tct ata tat caa aca aat   432

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63 Leu Gly Met Asn Pro Val Glu Glu Val Lys Ser Ile Tyr Gln Thr Asn
64     130             135                 140
66 cct aat gtt tgt ttt cat gta gtt tca ttt gca gat gat gct gaa ggc    480
67 Pro Asn Val Cys Phe His Val Val Ser Phe Ala Asp Asp Ala Glu Gly
68 145                 150                 155                 160
70 aaa gca ata att gat caa att gtt gca ctt aat agt gga agt gtt ctt    528
71 Lys Ala Ile Ile Asp Gln Ile Val Ala Leu Asn Ser Gly Ser Val Leu
72                 165                 170                 175
74 gtt gat ggt tta cag ctt cta caa aat cct gct gtt tgc caa gaa ttt    576
75 Val Asp Gly Leu Gln Leu Leu Gln Asn Pro Ala Val Cys Gln Glu Phe
76             180                 185                 190
78 gtt aat agt gtt ttt tgt caa gag caa att ctt gtt aca gaa gaa gtt    624
79 Val Asn Ser Val Phe Cys Gln Glu Gln Ile Leu Val Thr Glu Glu Val
80             195                 200                 205
82 gtt gta ctt cgt ggc gtc aac ttt gcc ttc ga                        656
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88 <211> LENGTH: 218
89 <212> TYPE: PRT
90 <213> ORGANISM: Lawsonia intracellularis
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96 Leu Val Asp Tyr Ser Gly Ser Met Met Lys His Val Ala Val Arg
97             20                  25                  30
99 Glu Pro Lys Ile Glu Leu Ala Lys Glu Ala Ile Leu Lys Ile Asn Ala
100            35                  40                  45
102 Ala Met Pro Lys Met Ser Tyr Gln Gly Gly Leu Tyr Thr Phe Ala Pro
103         50                  55                  60
105 Tyr Ser Val Ile Ile Pro Gln Gly Ser Trp Asn Ser Cys Val Ala Glu
106 65                  70                  75                  80
108 Cys Ala Val Asn Thr Ile Lys Ser Asp Leu Glu Ile Phe Gly Arg Leu
109                 85                  90                  95
111 Thr Pro Val Gly Asp Gly Ile Lys Met His Glu Thr Val Ile Asn Gln
112             100                 105                 110
114 Met Pro Pro Gln Ala Ala Val Ile Leu Leu Thr Asp Gly His Asn Asn
115         115                 120                 125
117 Leu Gly Met Asn Pro Val Glu Glu Val Lys Ser Ile Tyr Gln Thr Asn
118     130             135                 140
120 Pro Asn Val Cys Phe His Val Val Ser Phe Ala Asp Asp Ala Glu Gly
121 145                 150                 155                 160
123 Lys Ala Ile Ile Asp Gln Ile Val Ala Leu Asn Ser Gly Ser Val Leu
124                 165                 170                 175
126 Val Asp Gly Leu Gln Leu Leu Gln Asn Pro Ala Val Cys Gln Glu Phe
127             180                 185                 190
129 Val Asn Ser Val Phe Cys Gln Glu Gln Ile Leu Val Thr Glu Glu Val
130             195                 200                 205
132 Val Val Leu Arg Gly Val Asn Phe Ala Phe
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144 <222> LOCATION: (1)..(1425)
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149  1               5                  10                  15
151 caa caa tct agt ttt atg aag ggc gat gga gat caa cgt ttt tcg cct     96
152 Gln Gln Ser Ser Phe Met Lys Gly Asp Gly Asp Gln Arg Phe Ser Pro
153            20                  25                  30
155 aaa caa cgt tta cgt act caa ata gac att gtt gca tca gag agt ctt    144
156 Lys Gln Arg Leu Arg Thr Gln Ile Asp Ile Val Ala Ser Glu Ser Leu
157          35                  40                  45
159 aag ggt gtt gta ttc ttt gaa tta ggt aag act atc tgg gga cgt ggt    192
160 Lys Gly Val Val Phe Phe Glu Leu Gly Lys Thr Ile Trp Gly Arg Gly
161     50                  55                  60
163 gtt gat ggt gct tct att gga aca gat ggt aaa aat gtt ata aag ctc    240
164 Val Asp Gly Ala Ser Ile Gly Thr Asp Gly Lys Asn Val Ile Lys Leu
165 65                  70                  75                  80
167 cgt tat tcc tat gtt gat tgg gtt att cct tac aca gat gtg caa gtc    288
168 Arg Tyr Ser Tyr Val Asp Trp Val Ile Pro Tyr Thr Asp Val Gln Val
169                 85                  90                  95
171 cgt atg ggt tta caa cct tat gtc ctt cca gga ttt gtt gca ggt tct    336
172 Arg Met Gly Leu Gln Pro Tyr Val Leu Pro Gly Phe Val Ala Gly Ser
173            100                 105                .110
175 aca ata tta gat gct gat gga gca ggt gtt act gtt tct gct gta ttt    384
176 Thr Ile Leu Asp Ala Asp Gly Ala Gly Val Thr Val Ser Ala Val Phe
177          115                 120                 125
179 aat gat tat tta ggt gct aca gct ttc tgg atg cgt gca ttg cat aaa    432
180 Asn Asp Tyr Leu Gly Ala Thr Ala Phe Trp Met Arg Ala Leu His Lys
181      130                 135                 140
183 aac tat gat agt aat tat gga ata tca aag cta cct aac ttt aaa ggt    480
184 Asn Tyr Asp Ser Asn Tyr Gly Ile Ser Lys Leu Pro Asn Phe Lys Gly
185 145                 150                 155                 160
187 aca aca tta gat gta gtt gga tta act att cct gta aca ata tct gat    528
188 Thr Thr Leu Asp Val Val Gly Leu Thr Ile Pro Val Thr Ile Ser Asp
189                 165                 170                 175
191 ata aaa att gct cca tgg ggt atg ttt gct ttt gca ggt aag aag agc    576
192 Ile Lys Ile Ala Pro Trp Gly Met Phe Ala Phe Ala Gly Lys Lys Ser
193            180                 185                 190
195 tta tta ggg gaa agc tat gga gat att gaa gat gta aga gca ggt ctt    624
196 Leu Leu Gly Glu Ser Tyr Gly Asp Ile Glu Asp Val Arg Ala Gly Leu
197          195                 200                 205
199 tta cca gca atg cca gca gga ttt gga tat agc tgg gga gct ggt aat    672
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200 Leu Pro Ala Met Pro Ala Gly Phe Gly Tyr Ser Trp Gly Ala Gly Asn
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203 cca ttt gga gat gtt ttt cca aat aaa aag cgt ggt aat gca tgg tgg      720
204 Pro Phe Gly Asp Val Phe Pro Asn Lys Lys Arg Gly Asn Ala Trp Trp
205 225                 230                 235                 240
207 gtt ggt tta tca gct gaa ctt gct ggc tca agt cct ttg cat ata gct      768
208 Val Gly Leu Ser Ala Glu Leu Ala Gly Ser Ser Pro Leu His Ile Ala
209                 245                 250                 255
211 gtt gat ggt gct tat gga cga gca gac tta gga agt ctt aga aat gtt      816
212 Val Asp Gly Ala Tyr Gly Arg Ala Asp Leu Gly Ser Leu Arg Asn Val
213             260                 265                 270
215 gtt att ggt gac ttc tta cta gat aag att gat tta aaa cgt caa ggt      864
216 Val Ile Gly Asp Phe Leu Leu Asp Lys Ile Asp Leu Lys Arg Gln Gly
217             275                 280                 285
219 tgg tat gca gca tta tta gca gaa tat aaa ttt gaa tat gta act cca      912
220 Trp Tyr Ala Ala Leu Leu Ala Glu Tyr Lys Phe Glu Tyr Val Thr Pro
221     290                 295                 300
223 ggg gtt ata ggt tgg tat gcc tca gga gat aaa gtt gat tca cgt ggc      960
224 Gly Val Ile Gly Trp Tyr Ala Ser Gly Asp Lys Val Asp Ser Arg Gly
225 305                 310                 315                 320
227 gcc tct aaa aga ata cca aca tta gtt gga aac tgg tca gca aca agt     1008
228 Ala Ser Lys Arg Ile Pro Thr Leu Val Gly Asn Trp Ser Ala Thr Ser
229                 325                 330                 335
231 ttt gga tat agt gga gcc tat ggt ata ggc aaa gat tct gtt ttt gga     1056
232 Phe Gly Tyr Ser Gly Ala Tyr Gly Ile Gly Lys Asp Ser Val Phe Gly
233             340                 345                 350
235 aat act att gct ggc tca tgg ggt gtt gta gtt cag ttg aaa gat att     1104
236 Asn Thr Ile Ala Gly Ser Trp Gly Val Val Val Gln Leu Lys Asp Ile
237             355                 360                 365
239 tct ttc tta gaa aat cta act cat ggt atc cgt gga gct aga att cag     1152
240 Ser Phe Leu Glu Asn Leu Thr His Gly Ile Arg Gly Ala Arg Ile Gln
241     370                 375                 380
243 ggt aca aat aat aaa gac gtt cct gaa cac tta ggt tta tca tac gtt     1200
244 Gly Thr Asn Asn Lys Asp Val Pro Glu His Leu Gly Leu Ser Tyr Val
245 385                 390                 395                 400
247 act acc att tat gac aca cgt ggt ggt gat aat atg ctt tac tta aca     1248
248 Thr Thr Ile Tyr Asp Thr Arg Gly Gly Asp Asn Met Leu Tyr Leu Thr
249                 405                 410                 415
251 aag aaa gat tat gct tgg gaa gta gat ttt gat act gaa tat aaa atc     1296
252 Lys Lys Asp Tyr Ala Trp Glu Val Asp Phe Asp Thr Glu Tyr Lys Ile
253             420                 425                 430
255 tat aaa gac tta agt gta gct ctt gaa ctg tca tat att cgt ctt gaa     1344
256 Tyr Lys Asp Leu Ser Val Ala Leu Glu Leu Ser Tyr Ile Arg Leu Glu
257             435                 440                 445
259 ctt gat aaa aaa cta tgg aac ctt caa aga gaa gtt gat aag aat gcc     1392
260 Leu Asp Lys Lys Leu Trp Asn Leu Gln Arg Glu Val Asp Lys Asn Ala
261     450                 455                 460
263 tat cgt gct ggt tta aat atg aag tat caa ttc taa                     1428
264 Tyr Arg Ala Gly Leu Asn Met Lys Tyr Gln Phe
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265 465   470   475
268 <210> SEQ ID NO: 4
269 <211> LENGTH: 475
270 <212> TYPE: PRT
271 <213> ORGANISM: Lawsonia intracellularis
273 <400> SEQUENCE: 4
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278   20   25   30
280 Lys Gln Arg Leu Arg Thr Gln Ile Asp Ile Val Ala Ser Glu Ser Leu
281   35   40   45
283 Lys Gly Val Val Phe Phe Glu Leu Gly Lys Thr Ile Trp Gly Arg Gly
284   50   55   60
286 Val Asp Gly Ala Ser Ile Gly Thr Asp Gly Lys Asn Val Ile Lys Leu
287 65   70   75   80
289 Arg Tyr Ser Tyr Val Asp Trp Val Ile Pro Tyr Thr Asp Val Gln Val
290   85   90   95
292 Arg Met Gly Leu Gln Pro Tyr Val Leu Pro Gly Phe Val Ala Gly Ser
293   100   105   110
295 Thr Ile Leu Asp Ala Asp Gly Ala Gly Val Thr Val Ser Ala Val Phe
296   115   120   125
298 Asn Asp Tyr Leu Gly Ala Thr Ala Phe Trp Met Arg Ala Leu His Lys
299   130   135   140
301 Asn Tyr Asp Ser Asn Tyr Gly Ile Ser Lys Leu Pro Asn Phe Lys Gly
302 145   150   155   160
304 Thr Thr Leu Asp Val Val Gly Leu Thr Ile Pro Val Thr Ile Ser Asp
305   165   170   175
307 Ile Lys Ile Ala Pro Trp Gly Met Phe Ala Phe Ala Gly Lys Lys Ser
308   180   185   190
310 Leu Leu Gly Glu Ser Tyr Gly Asp Ile Glu Asp Val Arg Ala Gly Leu
311   195   200   205
313 Leu Pro Ala Met Pro Ala Gly Phe Gly Tyr Ser Trp Gly Ala Gly Asn
314   210   215   220
316 Pro Phe Gly Asp Val Phe Pro Asn Lys Lys Arg Gly Asn Ala Trp Trp
317 225   230   235   240
319 Val Gly Leu Ser Ala Glu Leu Ala Gly Ser Ser Pro Leu His Ile Ala
320   245   250   255
322 Val Asp Gly Ala Tyr Gly Arg Ala Asp Leu Gly Ser Leu Arg Asn Val
323   260   265   270
325 Val Ile Gly Asp Phe Leu Leu Asp Lys Ile Asp Leu Lys Arg Gln Gly
326   275   280   285
328 Trp Tyr Ala Ala Leu Leu Ala Glu Tyr Lys Phe Glu Tyr Val Thr Pro
329   290   295   300
331 Gly Val Ile Gly Trp Tyr Ala Ser Gly Asp Lys Val Asp Ser Arg Gly
332 305   310   315   320
334 Ala Ser Lys Arg Ile Pro Thr Leu Val Gly Asn Trp Ser Ala Thr Ser
335   325   330   335
337 Phe Gly Tyr Ser Gly Ala Tyr Gly Ile Gly Lys Asp Ser Val Phe Gly

VERIFICATION SUMMARY   DATE: 01/17/2002
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L:10 M:270 C: Current Application Number differs, Replaced Current Application Number